

1645

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/446,677  
 DATE: 09/06/2000  
 TIME: 11:01:37  
 Input Set : A:\Birkell.txt  
 Output Set: N:\CRF3\09062000\I446677.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:  
 5 (i) APPLICANT: BIRKELUND, Svend  
 6 CHRISTIANSEN, Gunna  
 7 HEBBSGAARD PEDERSEN, Anna-Sofie  
 8 MYGIND, Per  
 9 KNUDSEN, Katrine  
 11 (ii) TITLE OF INVENTION: SURFACE EXPOSED PROTEINS FROM CHLAMYDIA  
 12 PNEUMONIAE  
 14 (iii) NUMBER OF SEQUENCES: 30  
 16 (iv) CORRESPONDENCE ADDRESS:  
 17 (A) ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.  
 18 (B) STREET: 624 Ninth Street, N.W., Suite 300  
 19 (C) CITY: Washington  
 20 (D) STATE: D.C.  
 21 (E) COUNTRY: USA  
 22 (F) ZIP: 20001  
 24 (v) COMPUTER READABLE FORM:  
 25 (A) MEDIUM TYPE: Floppy disk  
 26 (B) COMPUTER: IBM PC compatible  
 27 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
 28 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30  
 30 (vi) CURRENT APPLICATION DATA:  
 C--> 31 (A) APPLICATION NUMBER: US/09/446,677  
 C--> 32 (B) FILING DATE: 24-Mar-2000  
 C--> 38 (vii) PRIOR APPLICATION DATA:  
 35 (A) APPLICATION NUMBER: PCT/DK98/00266  
 36 (B) FILING DATE: 19-JUN-1998  
 39 (A) APPLICATION NUMBER: DK 0744/97  
 40 (B) FILING DATE: 23-JUN-1997  
 42 (viii) ATTORNEY/AGENT INFORMATION:  
 43 (A) NAME: COOPER, Iver P.  
 44 (B) REGISTRATION NUMBER: 28,005  
 45 (C) REFERENCE/DOCKET NUMBER: BIRKELUND=1  
 47 (ix) TELECOMMUNICATION INFORMATION:  
 48 (A) TELEPHONE: 202-628-5197  
 49 (B) TELEFAX: 202-737-3528

Does Not Comply  
 Corrected Diskette Needed

See pp. 2, 4, 6

ERRORED SEQUENCES

498 (2) INFORMATION FOR SEQ ID NO: 3:  
 500 (i) SEQUENCE CHARACTERISTICS:  
 501 (A) LENGTH: 2815 base pairs  
 502 (B) TYPE: nucleic acid  
 503 (C) STRANDEDNESS: single  
 504 (D) TOPOLOGY: linear

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Enter "hard return"  
here to correct.

(ii) MOLECULE TYPE: Genomic DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

E--> 510

506	ATGAAATCGC AATTTTCCTG GTTAGTGCTC TCTTCGACAT TGGCATGTTT TACTAGTTGT	60	TCCACTGTTT TTGCTGCAAC TGCTGAAAT ATA	180
508	511 ACTAACACAG GCACCTATAC TCCTAAAAAT ACGACTACTG GAATAGACTA TACTCTGACA			240
	512 GGAGATATAA CTCGCAAAA CCTTGGGGAT TCGGCAGCTT TAACGAAGG TTGTTTTCT			300
	513 GACACTACCG AATCTTTAAG CTTTGCCGGT AAGGGGTACT CACTTTCTTT TTTAAATATT			360
	514 AAGTCTAGTG CTGAAGGCGC AGCACTTTCT GTTACAACAT ATAAAAATCT GTCGCTAACA			420
	515 GGATTTTCGA GTCTTACTTT CTTAGCGGCC CCATCATCGG TAATCACAAC CCCCTCAGGA			480
	516 AAAGGTGCGA TTAAATGTGG AGGGGATCTT ACATTTGATA ACAATGGAAC TATTTTATTT			540
	517 AAACAAGATT ACTGTGAGGA AAATGGCGGA GCCATTCTTA CCAAGAACTT TTCTTTGAAA			600
	518 AACAGCAGCG GATCGATTTC TTTTGAGGG AATAAATCGA GCGCAACAGG GAAAAAAGGT			660
	519 GGGGCTATTT GTGCTACTGG TACTGTAGAT ATTACAAATA ATACGGCTCC TACCTCTTC			720
	520 TCGAACAAATA TTGCTGAAGC TGCAGGTGGA GCTATAAATA GCACAGGAAA CTGTACAATT			780
	521 ACAGGGAATA CGTCTCTTGT ATTTCTGAA AATAGTGTGA CAGCGACCGC AGGAAATGGA			840
	522 GGAGCTCTTT CTGAGATGCG CGATGTTACC ATATCTGGGA ATCAGAGTGT AACTTTCTCA			900
	523 GGAACCAAG CTGTAGCTAA TGGCGGAGCC ATTTATGCTA AGAAGCTTAC ACTGGCTTCC			960
	524 GGGGGGGGGG GGGGTATCTC CTTTCTTAAC AATATAGTCC AAGGTACCAC TGCAGGTAAT			1020
	525 GGTGAGCCCA TTTCTATACT GGCAGCTGGA GAGTGTAGTC TTTGAGGAGA AGCAGGGGAC			1080
	526 ATTACCTTCA ATGGGAATGC CATTTGTGCA ACTACACCAC AAATACAAA AAGAAATCT			1140
	527 ATTGACATAG GATCTACTGC AAAGATCAGC AATTTACGTG CAATATCTGG GCATAGCATC			1200
	528 TTTTCTACG ATCCGATTAC TGCTAATACG TATAGTGGGT CGATTGTTTT TTCTGGTGAA			1260
	529 AATAAGGCTG ATGCAGGTAA TAGTACAGAT TATAGTGGGT CGATTGTTTT TTCTGGTGAA			1320
	530 AAGCTCTCTG AAGATGAAGC AAAAGTTGCA GACAACCTCA CTTCTACGCT GAAGCAGCCT			1380
	531 GTAACCTCTA CTGCAGGAAA TTTAGTACTT AAACGTGGTG TCACTCTCGA TACGAAAGGC			1440
	532 TTTACTCAGA CCGCGGGTTC CTCTGTTATT ATGGATGCGG GCACAACGTT AAAAGCAAGT			1500
	533 ACAGAGGAGG TCACCTTAAC AGGTCTTTCC ATTCCTGTAG ACTCTTTAGG CGAGGGTAAG			1560
	534 AAAGTTGTAA TTGCTGCTTC TGCAGCAAGT AAAAAATGTAG CCCTTAGTGG TCCGATTCTT			1620
	535 CTTTTGGATA ACCAAGGGAA TGCTTATGAA AATCAGACT TAGGAAAAAC TCAAGACTTT			1680
	536 TCATTTGTGC AGCTCTCTGC TCTGGGTACT GCAACAACCTA CAGATGTTCC AGCGGTTCTT			1740
	537 ACAGTAGCAA CTCTACGCA CTATGGGTAT CAAGGTACTT GGGGAATGAC TTGGGTTGAT			1800
	538 GATACCGCAA GCACTCCAAA GACTAAGACA GCGACATTAG CTTGGACCAA TACAGGCTAC			1860
	539 CTTCCGAATC CTGAGCGTCA AGGACCTTTA GTTCCTAATA GCCTTTGGGG ATCTTTTCA			1920
	540 GACATCCAAG CGATFCAAGG TGTCATAGAG AGAAGTGCTT TGACTCTTTG TTCAGATCGA			1980
	541 GGCTTCTGGG CTGCGGGAGT CGCCAATTC TTAGATAAAG ATAAGAAAGG GGAACACGC			2040
	542 AAATACCGTC ATAAATCTGG TGGATATGCT ATCGGAGGTG CAGCGCAAC TTGTTCTGAA			2100
	543 AACTTAATTA GCTTTGCCTT TTGCCAATC TTTGGTAGCG ATAAAGATTT CTTAGTCGCT			2160
	544 AAAAAATCATA CTGATACCTA TGCAGGAGCC TTCTATATCC AACACATTAC AGAATGTAGT			2220
	545 GGGTTCATAG GTTGCTCTTT AGATAAACTT CCTGGCTCTT GGAGTCATAA ACCCTCTGTT			2280
	546 TTAGAAGGGC AGCTCGCTTA TAGCCACGTC AGTAATGATC TGAAGACAAA GTATACTGCG			2340
	547 TATCTGAGG TGAAAGGTTT TTGGGGGAAT AATGCTTTTA ACATGATGTT GGGAGCTTCT			2400
	548 TCTCATTCTT ATCCTGAATA CCTGCATGTG TTTGATACCT ATGCTCCATA CATCAAATG			2460
	549 AATCTGACCT ATATACGTCA GGACAGCTTC TCGGAGAAAG GTACAGAAAG AAGATCTTTT			2520
	550 GATGACAGCA ACCTCTTCAA TTTATCTTTG CCTATAGGGG TGAAGTTTGA GAAGTTCTCT			2580
	551 GATTGTAATG ACTTTTCTTA TGATCTGACT TTATCCTATG TTCTGTATCT TATCCGCAAT			2640
	552 GATCCCAAT GCACTACAGC ACTTGTAATC AGCGGAGCCT CTGGGAAAC TTATGCCAAT			2700
	553 AACTTAGCAC GACAGGCCTT GCAAGTGCCT GCAGGCAGTC ACTACGCCTT CTCTCCTATG			2760
	554 TTTGAAGTGC TCGGCCAGTT TGTCTTTGAA GTTCGTGGAT CCTCAGGAT TTATAATGTA			2815
	555 GATCTTGGGG GTAAGTTCCA ATTTAGGAG CGTCTCTCAT GTCTCAGAAA TTCTG			

743 (2) INFORMATION FOR SEQ ID NO: 3:

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Input Set : A:\Birkell.txt  
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745 (i) SEQUENCE CHARACTERISTICS:  
 746 (A) LENGTH: 3052 base pairs → see p. 4  
 747 (B) TYPE: nucleic acid  
 748 (C) STRANDEDNESS: single  
 749 (D) TOPOLOGY: linear  
 751 (ii) MOLECULE TYPE: Genomic DNA  
 753 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
 755 ATGCGATTCTT CGCTCTGCGG ATTTCTCTCTA GTTTTTCTT TAACATTGCT CTCAGTCTTC 60  
 756 GACACTTCTT TGAGTGCTAC TACGATTCTT TTAACCCAG AAGATAGTT TCATGGAGAT 120  
 757 AGTCAGAATG CAGAACGTTT TTATAATGTT CAAGCTGGG ATGTCTATAG CCTTACTGGT 180  
 758 GATGTCTCAA TATCTAACGT CGATAACTCT GCATTAAATA AAGCTGCTT CAATGTGACC 240  
 759 TCAGGAAGTG TGACGTTGCG AGGAAATCAT CATGGGTTAT ATTTTAATAA TATTTCCTCA 300  
 760 GGAAGTACAA AGGAAGGGGC TGTACTTTGT TGCCAAGATC CTCAGCAAC GGCACGTTT 360  
 761 TCTGGGTTCT CCACGCTCTC TTTTATTCAG AGCCCCGAG ATATTAAAGA ACAGGGATGT 420  
 762 CTCTATTCAA AAAATGCAT TATGCTCTTA AACAAATTAT TAGTGCCTT TGAACAAAAC 480  
 763 CAAAGTAAGA CTAAGGCGG AGCTATTAGT GGGGCGAATG TTAATAAGT AGGCAACTAC 540  
 764 GATTCCGTTT CTTTCTATCA GAATGCAGCC ACTTTGGAG GTGCTATCCA TTCTTCAGGT 600  
 765 CCCCTACAGA TTGCAGTAAA TCAGGCAGAG ATAAGATTG CACAAAATAC TGCCAAGAAT 660  
 766 GGTCTCTGGG GGGCTTTGTA CTCCGATGGT GATATTGATA TTGATCAGAA TGCTTATGTT 720  
 767 CTATTTCCAG AAAATGAGG ATTGACTACT GCTATAGGTA AGGGAGGGG TGTCTGTTGT 780  
 768 CTTCCCACTT CAGGAAGTAG TACTCCAGTT CCTATTGTGA CTTTCTCTGA CAATAAACAG 840  
 769 TTAGTCTTTG AAAGAAACCA TTCCATAATG GGTGGCGGAG CCATTATATC TAGGAAACTT 900  
 770 AGCATCTCTT CAGGAGGTCC TACTCTATTT ATCAATAATA TATCATATGC AAATTCGCAA 960  
 771 AATTTAGGTG GAGCTATTGC CATTGATACT GGAGGGGAGA TCAGTTTATC AGCAGAGAAA 1020  
 772 GGAACAATTA CATTTCCAGG AAACCCGACG GCGAGAAATG GATGCTCTAT AGAATTTTAT 1080  
 773 TTACAAAATG CTAATTCCTT GAAATTACAG CAGGAGAAATG GATGCTCTAT AGAATTTTAT 1140  
 774 GATCCTATTA CTTCTGAAGC AGATGGGTCT ACCCAATTGA ATATCAACGG AGATCCTAAA 1200  
 775 AATAAAGAGT ACACAGGGAC CATACTCTTT TCTGGAGAAA AGAGTCTAGC AAACGATCCT 1260  
 776 AGGGATTTTA AATCTACAAT CCCTCAGAAC GTCAACCTGT CTGCAGGATA CTTAGTTATT 1320  
 777 AAAGAGGGGG CCGAAGTCAC AGTTTCAAAA TTCACGCAGT CTCCAGGATC GCATTTAGTT 1380  
 778 TTAGATTAGT GAACCAAACT GATAGCCTCT AAGGAAGACA TTGCCATCAC AGGCCTCGCG 1440  
 779 ATAGATATAG ATAGCTTAAG CTCATCCTCA ACAGCAGCTG TTATTAAGC AAACCCGCA 1500  
 780 AATAAACAGA TATCCGTGAC GGACTCTATA GAACTTATCT CGCCTACTGG CAATGCCTAT 1560  
 781 GAAGATCTCA AATGAGAGAA TTCACAGACG TTCCCTCTGC TCTCTTTAGA GCCTGGAGCC 1620  
 782 GGGGGTAGTG TGACTGTAAC TGCTGGAGAT TTCTTACCGG TAAGTCCCCA TTATGGTTT 1680  
 783 CAAGGCAATT GGAAATTAGC TTGGACAGGA ACTGGAAACA AAGTTGGAGA ATTCTTCTGG 1740  
 784 GATAAAATAA ATTATAAGCC TAGACCTGAA AAAGAAGGAA ATTTAGTTCC TAATATCTTG 1800  
 785 TGGGGGAATG CTGTAAATGT CAGATCCTTA ATGCAGGTTT AAGAGACCCA TGCAATCGAGC 1860  
 786 TTACAGACAG ATCGAGGGCT GTGGATCGAT GGAATTGGGA ATTTCTTCCA TGATCTGACC 1920  
 787 TCCGAAGACA ATATAAGGTA CCGTCATAAC AGCGGTGGAT ATGTTCTATC TGTAAATAAT 1980  
 788 GAGATCACAC CTAAGCATA TACTTCGATG GCATTTTCCC AACTCTTTAG TAGAGACAAG 2040  
 789 GACTATGCGG TTTCCAACAA CGAATACAGA ATGTATTAGT GATCGTATCT CTATCAATAT 2100  
 790 ACAACCTCCC TAGGGAATAT TTCCGTTAT GCTTCGCGTA ACCCTAATGT AAACGTCGGG 2160  
 791 ATTCTCTCAA GAAGGTTTCT TCAAAATCCT CTTATGATTT TTCATTTTTT GTGTGCTTAT 2220  
 792 GGTTCATGCCA CCAATGATAT GAAAACAGAC TACGCAAAAT TCCCTATGGT GAAAAACAGC 2280  
 793 TGGAGAAACA ATTGTTGGGC TATAGAGTGC GGAGGGAGCA TGCTCTATT GGTATTGAG 2340  
 794 AACGGAGAC TTTTCCAAGG TGCCATCCCA TTTATGAAAC TACAATTAGT TTATGCTTAT 2400  
 795 CAGGGAGATT TCAAAGAGAC GACTGCAGAT GGCCGTAGAT TTAGTAATGG GAGTTTAAAC 2460  
 796 TCGATTCTCT TACCTCTAGG CATACGCTTT GAGAAGCTGG CACTTTCTCA GGATGTACTC 2520

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```

797 TATGACTTTA GTTCTCTCCTA TATTCCTGAT ATTTTCCGTA AGGATCCCTC ATGTGAAGCT 2580
798 GCTCTGGTGA TTAGCGGAGA CTCCTGGCTT GTTCCGGCAG CACACGTATC AAGACATGCT 2640
799 TTTGTAGGGA GTGGAACGGG TCGGTATCAC TTTAACGACT ATACTGAGCT CTTATGTCGA 2700
800 GGAAGTATAG AATGCCGCCC CCATGCTAGG AATTATAATA TAAACTGTGG AAGCAAATTT 2760
801 CGTTTTTAGA AGGTTTCCAT TGCCTGTGTG GTTCCGGATC TTAACATAAA ATCCTGGACT 2820
802 ATGGATCATA GGCATTGGGT TTCTCGAAGT TGTGTGGAGA ATAACGACAT TTTATATGCA 2880
803 TAACGGAATA CTCGTATCAC CTCAGCCCCT AGAGACATTC TTTAGGGGTT CTTTATTGTT 2940
804 CTAACACTCG TATTTTATCG AGAATCCTTT ACGTTCTTGG TTTGCTTGTC TCCGAGGAGT 3000
E--> 805 TCCTTAACGA ATCATAGGGA TTCCAGGGTT CTGTTCCCTG AGTCCCTTGG A 3052
2597 (2) INFORMATION FOR SEQ ID NO: 24:
2599 (i) SEQUENCE CHARACTERISTICS:
2600 (A) LENGTH: 246 amino acids
2601 (B) TYPE: amino acid
2602 (C) STRANDEDNESS: single
2603 (D) TOPOLOGY: linear
2605 (ii) MOLECULE TYPE: peptide
2607 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:
2609 Met Lys Thr Ser Val Ser Met Leu Leu Ala Leu Leu Cys Ser Gly Ala
2610 1 5 10 15
2612 Ser Ser Ile Val Leu His Ala Ala Thr Thr Pro Leu Asn Pro Glu Asp
2613 20 25 30
2615 Gly Phe Ile Gly Glu Gly Asn Thr Asn Thr Phe Ser Pro Lys Ser Thr
2616 35 40 45
2618 Thr Asp Ala Ala Gly Thr Thr Tyr Ser Leu Thr Gly Glu Val Leu Phe
2619 50 55 60
2621 Ile Asp Pro Gly Lys Gly Gly Ser Ile Thr Gly Thr Cys Phe Val Glu
2622 65 70 75
2624 Thr Ala Gly Asp Leu Thr Phe Leu Gly Asn Gly Asn Thr Leu Lys Phe
2625 85 90 95
2627 Leu Ser Val Asp Ala Gly Ala Asn Ile Ala Val Ala His Val Gln Gly
2628 100 105 110
2630 Ser Lys Asn Leu Ser Phe Thr Asp Phe Leu Ser Leu Val Ile Thr Glu
2631 115 120 125
2633 Ser Pro Lys Ser Ala Val Ser Thr Gly Lys Gly Ser Leu Val Ser Ser
2634 130 135 140
2636 Gly Ala Val Gln Leu Gln Asp Ile Asn Thr Leu Val Leu Thr Ser Asn
2637 145 150 155
2639 Ala Ser Val Glu Asp Gly Gly Val Ile Lys Gly Asn Ser Cys Leu Ile
2640 165 170 175
2642 Gln Gly Ile Lys Asn Ser Ala Ile Phe Gly Gln Asn Thr Ser Ser Lys
2643 180 185 190
2645 Lys Gly Gly Ala Ile Ser Thr Thr Gln Gly Leu Thr Ile Glu Asn Asn
2646 195 200 205
2648 Leu Gly Thr Leu Lys Phe Asn Glu Asn Lys Ala Val Thr Ser Gly Gly
2649 210 215 220
2651 Ala Leu Asp Leu Gly Ala Ala Ser Thr Phe Thr Ala Asn His Glu Leu
2652 225 230 235
2654 Ile Phe Ser Gln Asn Lys Thr Ser Gly Asn Ala Ala Asn Gly Gly Ala
2655 245 250 255

```

Number of bases  
conflict; 3052  
listed, 3051 found.

→ See p. 6

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2657	Ile	Asn	Cys	Ser	Gly	Asp	Leu	Thr	Phe	Thr	Asp	Asn	Thr	Ser	Leu	Leu
2658				260					265						270	
2660	Leu	Gln	Glu	Asn	Ser	Thr	Met	Gln	Asp	Gly	Gly	Ala	Leu	Cys	Ser	Thr
2661				275					280						285	
2663	Gly	Thr	Ile	Ser	Ile	Thr	Gly	Ser	Asp	Ser	Ile	Asn	Val	Ile	Gly	Asn
2664				290					295						300	
2666	Thr	Ser	Gly	Gln	Lys	Gly	Gly	Ala	Ile	Ser	Ala	Ala	Ser	Leu	Lys	Ile
2667	305					310					315					320
2669	Leu	Gly	Gly	Gln	Gly	Gly	Ala	Leu	Phe	Ser	Asn	Asn	Val	Val	Thr	His
2670						325					330					335
2672	Ala	Thr	Pro	Leu	Gly	Gly	Ala	Ile	Phe	Ile	Asn	Thr	Gly	Gly	Ser	Leu
2673				340							345					350
2675	Gln	Leu	Phe	Thr	Gln	Gly	Gly	Asp	Ile	Val	Phe	Glu	Gly	Asn	Gln	Val
2676				355					360							365
2678	Thr	Thr	Thr	Ala	Pro	Asn	Ala	Thr	Thr	Lys	Arg	Asn	Val	Ile	His	Leu
2679				370					375							380
2681	Glu	Ser	Ser	Thr	Ala	Lys	Trp	Thr	Gly	Leu	Ala	Ala	Ser	Gln	Gly	Asn
2682	385						390									400
2684	Ile	Tyr	Phe	Tyr	Asp	Pro	Ile	Thr	Thr	Asn	Asp	Thr	Gly	Ala	Ser	Asp
2685						405					410					415
2687	Asn	Leu	Arg	Ile	Asn	Glu	Val	Ser	Ala	Asn	Gln	Lys	Leu	Ser	Gly	Ser
2688				420							425					430
2690	Ile	Val	Phe	Ser	Gly	Glu	Arg	Leu	Ser	Thr	Ala	Glu	Ala	Ile	Ala	Glu
2691				435					440							445
2693	Asn	Leu	Thr	Ser	Arg	Ile	Asn	Gln	Pro	Val	Thr	Leu	Val	Glu	Gly	Ser
2694				450					455							460
2696	Leu	Glu	Leu	Lys	Gln	Gly	Val	Thr	Leu	Ile	Thr	Gln	Gly	Phe	Ser	Gln
2697	465					470					475					480
2699	Glu	Pro	Glu	Ser	Thr	Leu	Leu	Leu	Asp	Leu	Gly	Thr	Ser	Leu	Gln	Ala
2700						485					490					495
2702	Ser	Thr	Glu	Asp	Ile	Val	Ile	Thr	Asn	Ser	Ser	Ile	Asn	Ala	Asp	Thr
2703				500							505					510
2705	Ile	Tyr	Gly	Lys	Asn	Pro	Ile	Asn	Ile	Val	Ala	Ser	Ala	Ala	Asn	Lys
2706				515					520							525
2708	Asn	Ile	Thr	Leu	Thr	Gly	Thr	Leu	Ala	Leu	Val	Asn	Ala	Asp	Gly	Ala
2709				530					535							540
2711	Leu	Tyr	Glu	Asn	His	Thr	Leu	Gln	Asp	Ser	Gln	Asp	Tyr	Ser	Phe	Val
2712	545					550						555				560
2714	Lys	Leu	Ser	Pro	Gly	Ala	Gly	Gly	Thr	Ile	Ile	Thr	Gln	Asp	Ala	Ser
2715						565						570				

TECH CENTER 1600/2300

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```

2730          645          650          655
2732 Gln Glu Arg Gly Val Trp Gly Ala Gly Ile Ala Asn Phe Leu His Arg
2733          660          665          670
2735 Asp Lys Ile Asn Glu His Gly Tyr Arg His Ser Gly Val Gly Tyr Leu
2736          675          680          685
2738 Val Gly Val Gly Thr His Ala Phe Ser Asp Ala Thr Ile Asn Ala Ala
2739          690          695          700
2741 Phe Cys Gln Leu Phe Ser Arg Asp Lys Asp Tyr Val Val Ser Lys Asn
2742 705          710          715          720
2744 His Gly Thr Ser Tyr Ser Gly Val Val Phe Leu Glu Asp Thr Leu Glu
2745          725          730          735
2747 Phe Arg Ser Pro Gln Gly Phe Tyr Thr Asp Ser Ser Ser Glu Ala Cys
2748          740          745          750
2750 Cys Asn Gln Val Val Thr Ile Asp Met Gln Leu Ser Tyr Ser His Arg
2751          755          760          765
2753 Asn Asn Asp Met Lys Thr Lys Tyr Thr Thr Tyr Pro Glu Ala Gln Gly
2754          770          775          780
2756 Ser Trp Ala Asn Asp Val Phe Gly Leu Glu Phe Gly Ala Thr Thr Tyr
2757 785          790          795          800
2759 Tyr Tyr Pro Asn Ser Thr Phe Leu Phe Asp Tyr Tyr Ser Pro Phe Leu
2760          805          810          815
2762 Arg Leu Gln Cys Thr Tyr Ala His Gln Glu Asp Phe Lys Glu Thr Gly
2763          820          825          830
2765 Gly Glu Val Arg His Phe Thr Ser Gly Asp Leu Phe Asn Leu Ala Val
2766          835          840          845
2768 Pro Ile Gly Val Lys Phe Glu Arg Phe Ser Asp Cys Lys Arg Gly Ser
2769          850          855          860
2771 Tyr Glu Leu Thr Leu Ala Tyr Val Pro Asp Val Ile Arg Lys Asp Pro
2772 865          870          875          880
2774 Lys Ser Thr Ala Thr Leu Ala Ser Gly Ala Thr Trp Ser Thr His Gly
2775          885          890          895
2777 Asn Asn Leu Ser Arg Gln Gly Leu Gln Leu Arg Leu Gly Asn His Cys
2778          900          905          910
2780 Leu Ile Asn Pro Gly Ile Glu Val Phe Ser His Gly Ala Ile Glu Leu
2781          915          920          925
2783 Arg Gly Ser Ser Arg Asn Tyr Asn Ile Asn Leu Gly Gly Lys Tyr Arg
2784          930          935          940
2786 Phe
E--> 2787 945

```

→ 945 amino acids found, 946 listed as length.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/446,677

DATE: 09/06/2000

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Input Set : A:\Birkell.txt

Output Set: N:\CRF3\09062000\I446677.raw

L:31 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
 L:32 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
 L:38 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]  
 L:510 M:320 E: (1) Wrong Nucleic Acid Designator, 2  
 L:805 M:254 E: No. of Bases conflict, Input:3052 Counted:3051 SEQ:5  
 L:805 M:204 E: No. of Bases differ, LENGTH:Input:3052 Counted:3051 SEQ:5  
 L:2454 M:220 C: Keyword misspelled or invalid format, [(ii) MOLECULE TYPE:]  
 L:2787 M:203 E: No. of Seq. differs, LENGTH:Input:946 Found:945 SEQ:24